



Sequence Listing

<110> Kainoh, Mie

Tanaka, Toshiaki

<120> Chimeric proteins, their heterodimer complexes, and platelet substitutes

<130> 1102-98

<141> 1998-09-29

<150> PCT/JP98/00370

<151> 1997-01-29

<150> JP 9-15118

<151> 1997-01-29

<150> JP 9-234544

<151> 1997-08-29

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TECH CENTER 16000/2500  
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Lys Leu Gly Gly Ile Val Leu Pro Asn Asp Gly Gln Cys His Leu Glu	
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gct gag cat aaa gaa tgt gtt cag tgc aga gcc ttc aat aaa gga gaa	1968
Ala Glu His Lys Glu Cys Val Gln Cys Arg Ala Phe Asn Lys Gly Glu	
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Lys Lys Asp Thr Cys Thr Gln Glu Cys Ser Tyr Phe Asn Ile Thr Lys	
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665

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670

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Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn

685

690

695

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Pro Glu Cys Pro Thr Gly Pro Glu Asp Pro Glu

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Glu Pro Lys Ser Cys Asp

715

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Lys Thr His Thr Cys Pro Pro Cys Pro

720

725

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Ala Pro Glu Leu Leu

730



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Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser	
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His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu	
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Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	
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Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn	
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Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro	
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Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu	
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ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc	3220
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys	

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Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser			
865	870	875	
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Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp			
880	885	890	895
tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc			3364
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser			
900	905	910	
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Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala			
915	920	925	
ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa			3460
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Linear

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Linear

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-20

-15

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-10

-5

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Gly Tyr Ala Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu

20

25

30

35



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40 45 50	
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Tyr Lys Cys Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn	
55 60 65	
ttg caa act tca aca agc att cca aat gtt act gag atg aaa acc aac	336
Leu Gln Thr Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn	
70 75 80	
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Met Ser Leu Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Gly Phe	
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ctc aca tgt ggt cct ctg tgg gca cag caa tgt ggg aat cag tat tac	432
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Thr Thr Gly Val Cys Ser Asp Ile Ser Pro Asp Phe Gln Leu Ser Ala	
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Val Val Cys Asp Glu Ser Asn Ser Ile Tyr Pro Trp Asp Ala Val Lys	
150 155 160	
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Asn Phe Leu Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys	
165 170 175	

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Gln	Thr	Ser	Gln	Tyr	Gly	Gly	Asp	Leu	Thr	Asn	Thr	Phe	Gly	Ala	Ile	
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Gln	Tyr	Ala	Arg	Lys	Tyr	Ala	Tyr	Ser	Ala	Ala	Ser	Gly	Gly	Arg	Arg	
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Ser	Ala	Thr	Lys	Val	Met	Val	Val	Val	Thr	Asp	Gly	Glu	Ser	His	Asp	
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Leu	Arg	Phe	Gly	Ile	Ala	Val	Leu	Gly	Tyr	Leu	Asn	Arg	Asn	Ala	Leu	
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gat	act	aaa	aat	tta	ata	aaa	gaa	ata	aaa	gcg	atc	gct	agt	att	cca	1008
Asp	Thr	Lys	Asn	Leu	Ile	Lys	Glu	Ile	Lys	Ala	Ile	Ala	Ser	Ile	Pro	
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Thr	Glu	Arg	Tyr	Phe	Phe	Asn	Val	Ser	Asp	Glu	Ala	Ala	Leu	Leu	Glu	
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aag gct ggg aca tta gga gaa caa att ttc agc att gaa ggt act gtt 1104

Lys Ala Gly Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val

325

330

335

caa gga gga gac aac ttt cag atg gaa atg tca caa gtg gga ttc agt 1152

Gln Gly Gly Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser

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350

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gca gat tac tct tct caa aat gat att ctg atg ctg ggt gca gtg gga 1200

Ala Asp Tyr Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly

360

365

370

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375

380

385

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390

395

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cac agt tca tat tta ggt tac tct gtg gct gca att tct act gga gaa 1344

His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu

405

410

415

agc act cac ttt gtt gct ggt gct cct cgg gca aat tat acc ggc cag 1392

Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln

420

425

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435

ata gtg cta tat agt gtg aat gag aat ggc aat atc acg gtt att cag 1440

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455

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Cys Gln Val Ala Ala Ser Gln Lys Ser Val Ala Cys Asp Val Gly Tyr	
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Pro Ala Leu Lys Arg Glu Gln Gln Val Thr Phe Thr Ile Asn Phe Asp	
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935 940 945

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965 970 975

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Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro	
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gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa	3973
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys	
1125	1130
1135	
ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg	4021



Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val	
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1150	
gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac	4069
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr	
1155	1160
1165	
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Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu	
1170	1175
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cag tac aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac	4165
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His	
1190	1195
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Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys	
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gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa	4255
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys	
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Gly Gln Pro Arg Glu Pro	
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cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag	4417
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln	
1240	1245
1250	
gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc	4465
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala	

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Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr			
1270	1275	1280	1285
cct ccc gtg ctg gat tcc gac ggc tcc ttc ttc ctc tac agc aag ctc			4561
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu			
	1290	1295	1300
acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc			4609
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser			
	1305	1310	1315
gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc			4657
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser			
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Leu Ser Pro Gly Lys			

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